

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/791,017B  
Source: 1Fw/16  
Date Processed by STIC: 5/30/06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

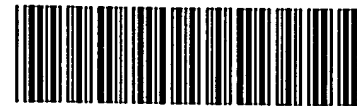
Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06



IFW16

## RAW SEQUENCE LISTING

DATE: 05/30/2006

PATENT APPLICATION: US/10/791,017B

TIME: 11:30:26

Input Set : A:\textobendorffsequence052006.txt

Output Set: N:\CRF4\05302006\J791017B.raw

4 <110> APPLICANT: JENAPHARM GmbH & Co. KG  
W--> 5 <120> TITLE OF INVENTION: Methods for Determining Hormonal Effects of Substances  
W--> 6 <130> FILE REFERENCE: Pat 3684/11  
W--> 7 <140> CURRENT APPLICATION NUMBER: US/10/791,017B  
8 <141> CURRENT FILING DATE: 2004-03-02  
E--> 10 <160> NUMBER OF SEQ ID NOS: 78 (see below) *see pp 1-5*  
11 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORRED SEQUENCES

404 <210> SEQ ID NO: 8 *last sequence in submitted file*  
405 <211> LENGTH: 918  
406 <212> TYPE: PRT  
407 <213> ORGANISM: Homo sapiens  
409 <400> SEQUENCE: 8  
412 Met Glu Val Gln Leu Gly Leu Gly Arg Val Tyr Pro Arg Pro Pro Ser  
413 1 5 10 15  
415 Lys Thr Tyr Arg Gly Ala Phe Gln Asn Leu Phe Gln Ser Val Arg Glu  
416 20 25 30  
418 Val Ile Gln Asn Pro Gly Pro Arg His Pro Glu Ala Ala Ser Ala Ala  
419 35 40 45  
421 Pro Pro Gly Ala Ser Leu Leu Leu Gln Gln Gln Gln Gln Gln  
422 50 55 60  
424 Gln Gln Gln Gln Gln Gln Gln Gln Gln Glu Thr Ser Pro Arg Gln  
425 65 70 75 80  
427 Gln Gln Gln Gln Gln Gln Glu Asp Gly Ser Pro Gln Ala His Arg Arg  
E--> 428 ~~85~~ 85 ~~90~~ 90 ~~95~~ 95 *misaligned amino acid numbers. Do not use TAB codes.*  
430 Gly Pro Thr Gly Tyr Leu Val Leu Asp Glu Glu Gln Gln Pro Ser Gln  
E--> 431 100 105 110  
433 Pro Gln Ser Ala Leu Glu Cys His Pro Glu Arg Gly Cys Val Pro Glu  
E--> 434 115 120 125  
436 Pro Gly Ala Ala Val Ala Ala Ser Lys Gly Leu Pro Gln Gln Leu Pro  
E--> 437 130 135 140  
439 Ala Pro Pro Asp Glu Asp Asp Ser Ala Ala Pro Ser Thr Leu Ser Leu  
E--> 440 145 150 155 160  
442 Leu Gly Pro Thr Phe Pro Gly Leu Ser Ser Cys Ser Ala Asp Leu Lys  
E--> 443 165 170 175  
445 Asp Ile Leu Ser Glu Ala Ser Thr Met Gln Leu Leu Gln Gln Gln  
E--> 446 180 185 190  
448 Gln Glu Ala Val Ser Glu Gly Ser Ser Gly Arg Ala Arg Glu Ala  
E--> 449 195 200 205  
451 Ser Gly Ala Pro Thr Ser Ser Lys Asp Asn Tyr Leu Gly Gly Thr Ser

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```

E--> 452      210      215      220
      454 Thr Ile Ser Asp Asn Ala Lys Glu Leu Cys Lys Ala Val Ser Val Ser
E--> 455 225      230      235      240
      457 Met Gly Leu Gly Val Glu Ala Leu Glu His Leu Ser Pro Gly Glu Gln
E--> 458      245      250      255
      460 Leu Arg Gly Asp Cys Met Tyr Ala Pro Leu Leu Gly Val Pro Pro Ala
E--> 461      260      265      270
      463 Val Arg Pro Thr Pro Cys Ala Pro Leu Ala Glu Cys Lys Gly Ser Leu
E--> 464      275      280      285
      466 Leu Asp Asp Ser Ala Gly Lys Ser Thr Glu Asp Thr Ala Glu Tyr Ser
E--> 467      290      295      300
      469 Pro Phe Lys Gly Gly Tyr Thr Lys Gly Leu Glu Gly Glu Ser Leu Gly
E--> 470 305      310      315      320
      472 Cys Ser Gly Ser Ala Ala Ala Gly Ser Ser Gly Thr Leu Glu Leu Pro
E--> 473      325 invalid      330      335
E--> 475 Ser Thr Leu Ser Ley Tyr Lys Ser Gly Ala Leu Asp Glu Ala Ala Ala
E--> 476      340      345      350
      478 Tyr Gln Ser Arg Asp Tyr Tyr Asn Phe Pro Leu Ala Leu Ala Gly Pro
E--> 479 355 355      360 360      365 365
      481 Pro Pro Pro Pro Pro Pro Pro His Pro His Ala Arg Ile Lys Leu Glu
E--> 482      370      375      380
      484 Asn Pro Leu Asp Tyr Gly Ser Ala Trp Ala Ala Ala Ala Ala Gln Cys
E--> 485 385      390      395      400
      487 Arg Tyr Gly Asp Leu Ala Ser Leu His Gly Ala Gly Ala Ala Gly Pro
E--> 488      405      410      415
      490 Gly Ser Gly Ser Pro Ser Ala Ala Ala Ser Ser Ser Trp His Thr Leu
E--> 491      420      425      430
      493 Phe Thr Ala Glu Glu Gly Gln Leu Tyr Gly Pro Cys Gly Gly Gly Gly
E--> 494      435      440      445
      496 Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly
E--> 497      450      455      460
      499 Gly Gly Gly Gly Gly Gly Gly Glu Ala Glu Ala Val Ala Pro Tyr Gly
E--> 500 465      470      475      480
      502 Tyr Thr Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe Thr
E--> 503      485      490      495
      505 Ala Pro Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro Tyr
E--> 506      500      505      510
      508 Pro Ser Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp Ser
E--> 509      515      520      525
E--> 511 Tyr Ser Gly Pro Tyr Gly Asp Met Arg Ley Glu Thr Ala Arg Asp His
E--> 512      530      535      540
      514 Val Leu Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile
E--> 515 545      550      555      560
      517 Cys Gly Asp Glu Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly
E--> 518      565      570      575
      520 Ser Cys Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr
E--> 521      580      585      590
      523 Leu Cys Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys
E--> 524      595      600      605

```

OK

invalid  
amino acid  
designator  
misaligned  
nos.

OK

invalid  
amino acid  
designator

OK

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526 Asn Cys Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr  
 E--> 527 610 615 620  
 529 Leu Gly Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu  
 E--> 530 625 630 635 640  
 532 Glu Gly Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr Gln  
 E--> 533 645 650 655  
 535 Lys Leu Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe  
 E--> 536 660 665 670  
 538 Leu Asn Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His  
 E--> 539 ~~675~~ 675 ~~680~~ 680 ~~685~~ 685  
 541 Asp Asn Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn  
 E--> 542 690 695 700  
 544 Glu Leu Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala  
 E--> 545 705 710 715 720  
 547 Leu Pro Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile  
 E--> 548 725 730 735  
 550 Gln Tyr Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser  
 E--> 551 740 745 750  
 553 Phe Thr Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val  
 E--> 554 755 760 765  
 556 Phe Asn Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val  
 E--> 557 770 775 780  
 559 Arg Met Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro  
 E--> 560 785 790 795 800  
 562 Gln Glu Phe Leu Cys Met Lys Ala Leu Leu Leu Phe Ser Ile Ile Pro  
 E--> 563 805 810 815  
 565 Val Asp Glu Leu Arg Met Asn Tyr Ile Lys Glu Leu Asp Arg Met Asn  
 E--> 566 820 825 830  
 568 Tyr Ile Lys Leu Glu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro  
 E--> 569 835 840 845  
 571 Thr Ser Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser  
 E--> 572 850 855 860  
 574 Val Gln Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu  
 E--> 575 865 870 875 880  
 577 Ile Lys Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu  
 E--> 578 885 890 895  
 580 Ile Ile Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro  
 E--> 581 ~~897~~ 900 905 910  
 584 Ile Tyr Phe His Thr Gln  
 E--> 585 ~~915~~ 915

OK

misaligned  
nos.

OK

delete this- Per sequence rules (1.822),  
 number the amino acids under  
 every 5 amino acids.

10/791, 017B

4

<210> 1  
<211> 2390  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (44)..(2011)  
<223> EWS

<400> 1  
agaggagac ggacgttgag agaacgagga ggaaggagag aaa atg gcg tcc acg 55  
Met Ala Ser Thr

→ 1 ← move the "1" directly

gat tac agt acc tat agc caa gct gca gcg cag cag ggc tac agt gct 103  
Asp Tyr Ser Thr Tyr Ser Gln Ala Ala Ala Gln Gln Gly Tyr Ser Ala  
5 10 15 20

under the  
"1" since  
the other  
number is  
under the  
last letter  
of amino acid

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/791,017B

DATE: 05/30/2006  
TIME: 11:30:27

FYI

Input Set : A:\textobendorfsequence052006.txt  
Output Set: N:\CRF4\05302006\J791017B.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:1; Line(s) 25

## VERIFICATION SUMMARY

DATE: 05/30/2006

PATENT APPLICATION: US/10/791,017B

TIME: 11:30:27

Input Set : A:\textobendorffsequence052006.txt

Output Set: N:\CRF4\05302006\J791017B.raw

L:5 M:283 W: Missing Blank Line separator, <120> field identifier  
L:6 M:283 W: Missing Blank Line separator, <130> field identifier  
L:7 M:283 W: Missing Blank Line separator, <140> field identifier  
L:26 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1  
L:428 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
M:332 Repeated in SeqNo=8  
L:475 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:511 M:330 E: (2) Invalid Amino Acid Designator, NUMBER OF INVALID KEYS:1  
L:10 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (7) Counted (8)